```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Waximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM nucleic - nucleic search, using sw model
GenEmbl:*
1: gb_bal:
2: gb_ba2:
3: gb_om:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             December 2, 2000, 14:54:45; Search time 10764.3 Seconds (without alignments) 2150.454 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-358-322-1
5300
1 gatcamatamaatgamacca.....taccatttacttacctgatc 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1033670 segs, 2183789903 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_pat:
gb_pl1:
gb_pl2:
gb_pr2:
gb_pr3:
gb_pr3:
gb_ro:
gb_ro:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                       em_on:
em_or:
em_ov:
em_ph:
em_ph:
em_ph:
em_to:
em_sy:
em_vi:
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em_hum2:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_in: •
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2067340
```

| 99999999999999999999999999999999999999 | 888877775687 | 0.000000000000000000000000000000000000 | 5 5 5 4 |
|---|--------------|--|---------|
| 9b_htg11: * 9b_htg19: * 9b_htg19: * 9b_htg20: * 9b_htg21: * 9b_htg22: * 9b_htg22: * 9b_htg23: * 9b_sts2: * 9b_sts2: * 9b_vi1: * 9b_vi1: * | blace | To read of the control of the contro | واواوا |
| | | | |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Score | Query | Query Match Length DB | 93 | ID | Description |
|--------------|-------|-------|--------------------------|--------|-----------|--------------------|
| 1 | 314.6 | | 1306 | 2 | CRPCS20 | X58242 C.ruminanti |
| N | 155.2 | | 312430 | N | RPXX02 | AJ235271 Rickettsi |
| w | 149.2 | | 14001 | ų. | PECOMPIRB | X95276 P.falciparu |
| 4 | 144.8 | | 69034 | 31 | AF007261 | AF007261 Reclinomo |
| U I | 140.6 | | 317511 | N | CJ11168X3 | AL139076 Campyloba |
| 6 | 138.2 | | 19517 | u S | DMU37541 | U37541 Drosophila |
| 7 | 137.6 | | 4601 | u u | DM011584 | Ull584 Drosophila |
| & | 136.2 | | 104992 | 68 | AC005504 | AC005504 Plasmodiu |
| ი 9 | 136.2 | | 163226 | 68 | AC004157 | AC004157 Plasmodiu |
| c 10 | 133.2 | | 14867 | 32 | AE001398 | AE001398 Plasmodiu |
| c 11 | 128.4 | ۵.4 | 86827 | w w | PFMAL3P5 | AL034556 Plasmodiu |
| . 12 | 124.2 | | 86827 | 33 | PEMAL3P5 | AL034556 Plasmodiu |